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1635

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/603,124B

DATE: 04/26/2001

TIME: 13:10:35

Input Set : D:\seqlistcorrected2.txt

Output Set: N:\CRF3\04262001\I603124B.raw

#9/K.T.
5/4
Raw
ENTERED seq.
see p.5 listing
(entered)

3 <110> APPLICANT: Pompejus, Markus
4 Kroger, Burkhard
5 Schroder, Hartwig
6 Zelder, Oskar
7 Haberhauer, Gregor
9 <120> TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
10 INVOLVED IN HOMEOSTASIS AND ADAPTATION
12 <130> FILE REFERENCE: BGI-132CP
14 <140> CURRENT APPLICATION NUMBER: 09/603124B
15 <141> CURRENT FILING DATE: 2000-06-23
17 <150> PRIOR APPLICATION NUMBER: US 60/141031
18 <151> PRIOR FILING DATE: 1999-06-25
20 <150> PRIOR APPLICATION NUMBER: US 60/143694
21 <151> PRIOR FILING DATE: 1999-07-14
23 <150> PRIOR APPLICATION NUMBER: US 60/151778
24 <151> PRIOR FILING DATE: 1999-08-31
26 <150> PRIOR APPLICATION NUMBER: DE 19931418.7
27 <151> PRIOR FILING DATE: 1999-07-08
29 <150> PRIOR APPLICATION NUMBER: DE 19932124.8
30 <151> PRIOR FILING DATE: 1999-07-09
32 <150> PRIOR APPLICATION NUMBER: DE 19932126.4
33 <151> PRIOR FILING DATE: 1999-07-09
35 <150> PRIOR APPLICATION NUMBER: DE 19932127.2
36 <151> PRIOR FILING DATE: 1999-07-09
38 <150> PRIOR APPLICATION NUMBER: DE 19932133.7
39 <151> PRIOR FILING DATE: 1999-07-09
41 <150> PRIOR APPLICATION NUMBER: DE 19932207.4
42 <151> PRIOR FILING DATE: 1999-07-09
44 <150> PRIOR APPLICATION NUMBER: DE 19932208.2
45 <151> PRIOR FILING DATE: 1999-07-09
47 <150> PRIOR APPLICATION NUMBER: DE 19932225.2
48 <151> PRIOR FILING DATE: 1999-07-09
50 <150> PRIOR APPLICATION NUMBER: DE 19932229.5
51 <151> PRIOR FILING DATE: 1999-07-09
53 <150> PRIOR APPLICATION NUMBER: DE 19932914.1
54 <151> PRIOR FILING DATE: 1999-07-14
56 <150> PRIOR APPLICATION NUMBER: DE 19933006.9
57 <151> PRIOR FILING DATE: 1999-07-14
59 <150> PRIOR APPLICATION NUMBER: DE 19940765.7
60 <151> PRIOR FILING DATE: 1999-08-27
62 <150> PRIOR APPLICATION NUMBER: DE 19940768.1
63 <151> PRIOR FILING DATE: 1999-08-27
65 <150> PRIOR APPLICATION NUMBER: DE 19940831.9
66 <151> PRIOR FILING DATE: 1999-08-27
68 <150> PRIOR APPLICATION NUMBER: DE 19940832.7
69 <151> PRIOR FILING DATE: 1999-08-27
71 <150> PRIOR APPLICATION NUMBER: DE 19941385.1

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72 <151> PRIOR FILING DATE: 1999-08-31
74 <150> PRIOR APPLICATION NUMBER: DE 19941396.7
75 <151> PRIOR FILING DATE: 1999-08-31
77 <150> PRIOR APPLICATION NUMBER: DE 19942087.4
78 <151> PRIOR FILING DATE: 1999-09-03
80 <160> NUMBER OF SEQ ID NOS: 480
82 <210> SEQ ID NO: 1
83 <211> LENGTH: 1581
84 <212> TYPE: DNA
85 <213> ORGANISM: Corynebacterium glutamicum
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (101)..(1558)
90 <223> OTHER INFORMATION: RXA02702
92 <400> SEQUENCE: 1
93 gcaggtaacg cctccacggt gattgcagac atgattgctg caactatcaa tagccaacac 60
95 aactaaaacg accagctcaa cgcaaaggaa tagtttaag'gtg acc act cca cac 115
96                                     Val Thr Thr Pro His
97                                     1           5
99 ttg gat tct gca caa gat att gat ctg tcc cgc gtc cac ctc atc ggt 163
100 Leu Asp Ser Ala Gln Asp Ile Asp Leu Ser Arg Val His Leu Ile Gly
101                                     10           15           20
103 att ggc gga gcc gga atg tct ggc gtt gcc cga atc ctg ctt gcc cgc 211
104 Ile Gly Gly Ala Gly Met Ser Gly Val Ala Arg Ile Leu Leu Ala Arg
105                                     25           30           35
107 ggt aag aca gtc act ggt tcc gat gcc aaa gat tcc cgc acc ttg ctt 259
108 Gly Lys Thr Val Thr Gly Ser Asp Ala.Lys Asp Ser Arg Thr Leu Leu
109                                     40           45           50
111 cca ctc cgc gcc gtg gga gcc acc atc gca gtg gga cac gct gcg gaa 307
112 Pro Leu Arg Ala Val Gly Ala Thr Ile Ala Val Gly His Ala Ala Glu
113                                     55           60           65
115 aac ctt gag ctt tcc ggc gaa ctt ccc acc gtc gtg gtg acc tct ttt 355
116 Asn Leu Glu Leu Ser Gly Glu Leu Pro Thr Val Val Val Thr Ser Phe
117 70           75           80           85
119 gcc gcc att ccg caa gac aac ccg gaa ctt gtt cgt gca cgt gaa gaa 403
120 Ala Ala Ile Pro Gln Asp Asn Pro Glu Leu Val Arg Ala Arg Glu Glu
121                                     90           95           100
123 ggc att ccg gtt att cgt cgc tcc gat ctg ttg ggc gaa ttg ctg gaa 451
124 Gly Ile Pro Val Ile Arg Arg Ser Asp Leu Leu Gly Glu Leu Leu Glu
125                                     105          110          115
127 ggc tcc acc cag gtc ttg atc gcg ggt acc cac ggt aag acc tcc acc 499
128 Gly Ser Thr Gln Val Leu Ile Ala Gly Thr His Gly Lys Thr Ser Thr
129                                     120          125          130
131 acc tct atg tct gtg gta gct atg cag gca gcg ggc atg gat cca agc 547
132 Thr Ser Met Ser Val Val Ala Met Gln Ala Ala Gly Met Asp Pro Ser
133                                     135          140          145
135 ttt gct atc ggc gga cag ctc aac aag gct ggc acc aat gcg cac cat 595
136 Phe Ala Ile Gly Gly Gln Leu Asn Lys Ala Gly Thr Asn Ala His His
137 150           155           160           165

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139	gga act ggt gag gtc ttt atc gct gaa gca gat gaa tct gac gca tcg	
140	Gly Thr Gly Glu Val Phe Ile Ala Glu Ala Asp Glu Ser Asp Ala Ser	
141	170 175 180	
143	ctg ctg cgc tac aag cca aat gtt gca gtg gtc acc aat gtg gaa cca	691
144	Leu Leu Arg Tyr Lys Pro Asn Val Ala Val Val Thr Asn Val Glu Pro	
145	185 190 195	
147	gac cac ctg gac ttc ttt aaa acc cct gaa gcc tac ttc caa gtg ttc	739
148	Asp His Leu Asp Phe Phe Lys Thr Pro Glu Ala Tyr Phe Gln Val Phe	
149	200 205 210	
151	gac gat ttc gca gga cgc atc acc ccg aac ggc aag ctg gtt gtg tgc	787
152	Asp Asp Phe Ala Gly Arg Ile Thr Pro Asn Gly Lys Leu Val Val Cys	
153	215 220 225	
155	ctg aac gat cct cac gca gcg gag ctg ggg gag agg tct gtc cgc aag	835
156	Leu Asn Asp Pro His Ala Ala Glu Leu Gly Glu Arg Ser Val Arg Lys	
157	230 235 240 245	
159	ggt atc aag act gtt ggt tac ggt acc gct gac gcc gta cag gca cac	883
160	Gly Ile Lys Thr Val Gly Tyr Gly Thr Ala Asp Ala Val Gln Ala His	
161	250 255 260	
163	cct gag gtt cca gcg atg gct acc atc gtg gat tcc caa gtt gtc gca	931
164	Pro Glu Val Pro Ala Met Ala Thr Ile Val Asp Ser Gln Val Val Ala	
165	265 270 275	
167	gaa ggc acc cgc gcc acc atc aac atc gat gga cag gaa gta tct gtg	979
168	Glu Gly Thr Arg Ala Thr Ile Asn Ile Asp Gly Gln Glu Val Ser Val	
169	280 285 290	
171	att ctt caa atc cct ggt gat cac atg gta ctc aac ggt gca gcc gcc	1027
172	Ile Leu Gln Ile Pro Gly Asp His Met Val Leu Asn Gly Ala Ala Ala	
173	295 300 305	
175	ctg ctg gcc gga tac ctg gtg ggt ggg gac gtc gac aag ctt gtt gaa	1075
176	Leu Leu Ala Gly Tyr Leu Val Gly Gly Asp Val Asp Lys Leu Val Glu	
177	310 315 320 325	
179	ggc ttg tcg gat ttc tcc ggc gtg cga cgc cgc ttt gag ttc cac ggt	1123
180	Gly Leu Ser Asp Phe Ser Gly Val Arg Arg Arg Phe Glu Phe His Gly	
181	330 335 340	
183	gct atc gag ggc ggc aaa ttt aat ggc gct gct att tat gat gat tac	1171
184	Ala Ile Glu Gly Lys Phe Asn Gly Ala Ala Ile Tyr Asp Asp Tyr	
185	345 350 355	
187	gca cac cac cca acg gaa gta act gca gtg ctc agc gct gcg cgc acc	1219
188	Ala His His Pro Thr Glu Val Thr Ala Val Leu Ser Ala Ala Arg Thr	
189	360 365 370	
191	cgg gtg aag gcc gct gga aag ggc cgt gtc atc gtc gcg ttc caa cca	1267
192	Arg Val Lys Ala Ala Gly Lys Gly Arg Val Ile Val Ala Phe Gln Pro	
193	375 380 385	
195	cat tta tac tca cgc acc ata gaa ttc caa aag gag ttc gcg ggg gca	1315
196	His Leu Tyr Ser Arg Thr Ile Glu Phe Gln Lys Glu Phe Ala Gly Ala	
197	390 395 400 405	
199	ctg tca ctg gca gac gct gcc gtg gtg ctt gag att tac gga gcg cgc	1363
200	Leu Ser Leu Ala Asp Ala Ala Val Val Leu Glu Ile Tyr Gly Ala Arg	
201	410 415 420	
203	gaa caa ccg gtg gat ggc gtg tcc tcg gaa atc atc acc gat gcg atg	1411

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204 Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile Ile Thr Asp Ala Met
205          425          430          435
207 acc att cca gtg gtg tac gaa cct aat ttc tct gca gtc cca gaa cgc 1459
208 Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser Ala Val Pro Glu Arg
209          440          445          450
211 att gca gaa atc gca gga cct aat gac atc gtg ctc acc atg ggt gca 1507
212 Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val Leu Thr Met Gly Ala
213          455          460          465
215 ggt tcc gtg acc atg ctt gct cca gaa atc ctg gat cag ctg caa aac 1555
216 Gly Ser Val Thr Met Leu Ala Pro Glu Ile Leu Asp Gln Leu Gln Asn
217 470          475          480          485
219 aat taggacgtaa gtgaacaagg cag 1581
220 Asn
224 <210> SEQ ID NO: 2
225 <211> LENGTH: 486
226 <212> TYPE: PRT
227 <213> ORGANISM: Corynebacterium glutamicum
229 <400> SEQUENCE: 2
230 Val Thr Thr Pro His Leu Asp Ser Ala Gln Asp Ile Asp Leu Ser Arg
231 1 5 10 15
233 Val His Leu Ile Gly Ile Gly Gly Ala Gly Met Ser Gly Val Ala Arg
234 20 25 30
236 Ile Leu Leu Ala Arg Gly Lys Thr Val Thr Gly Ser Asp Ala Lys Asp
237 35 40 45
239 Ser Arg Thr Leu Leu Pro Leu Arg Ala Val Gly Ala Thr Ile Ala Val
240 50 55 60
242 Gly His Ala Ala Glu Asn Leu Glu Leu Ser Gly Glu Leu Pro Thr Val
243 65 70 75 80
245 Val Val Thr Ser Phe Ala Ala Ile Pro Gln Asp Asn Pro Glu Leu Val
246 85 90 95
248 Arg Ala Arg Glu Glu Gly Ile Pro Val Ile Arg Arg Ser Asp Leu Leu
249 100 105 110
251 Gly Glu Leu Leu Glu Gly Ser Thr Gln Val Leu Ile Ala Gly Thr His
252 115 120 125
254 Gly Lys Thr Ser Thr Thr Ser Met Ser Val Val Ala Met Gln Ala Ala
255 130 135 140
257 Gly Met Asp Pro Ser Phe Ala Ile Gly Gly Gln Leu Asn Lys Ala Gly
258 145 150 155 160
260 Thr Asn Ala His His Gly Thr Gly Glu Val Phe Ile Ala Glu Ala Asp
261 165 170 175
263 Glu Ser Asp Ala Ser Leu Leu Arg Tyr Lys Pro Asn Val Ala Val Val
264 180 185 190
266 Thr Asn Val Glu Pro Asp His Leu Asp Phe Phe Lys Thr Pro Glu Ala
267 195 200 205
269 Tyr Phe Gln Val Phe Asp Asp Phe Ala Gly Arg Ile Thr Pro Asn Gly
270 210 215 220
272 Lys Leu Val Val Cys Leu Asn Asp Pro His Ala Ala Glu Leu Gly Glu
273 225 230 235 240
275 Arg Ser Val Arg Lys Gly Ile Lys Thr Val Gly Tyr Gly Thr Ala Asp

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276          245          250          255
278 Ala Val Gln Ala His Pro Glu Val Pro Ala Met Ala Thr Ile Val Asp
279          260          265          270
281 Ser Gln Val Val Ala Glu Gly Thr Arg Ala Thr Ile Asn Ile Asp Gly
282          275          280          285
284 Gln Glu Val Ser Val Ile Leu Gln Ile Pro Gly Asp His Met Val Leu
285          290          295          300
287 Asn Gly Ala Ala Ala Leu Leu Ala Gly Tyr Leu Val Gly Gly Asp Val
288 305          310          315          320
290 Asp Lys Leu Val Glu Gly Leu Ser Asp Phe Ser Gly Val Arg Arg Arg
291          325          330          335
293 Phe Glu Phe His Gly Ala Ile Glu Gly Gly Lys Phe Asn Gly Ala Ala
294          340          345          350
296 Ile Tyr Asp Asp Tyr Ala His His Pro Thr Glu Val Thr Ala Val Leu
297          355          360          365
299 Ser Ala Ala Arg Thr Arg Val Lys Ala Ala Gly Lys Gly Arg Val Ile
300          370          375          380
302 Val Ala Phe Gln Pro His Leu Tyr Ser Arg Thr Ile Glu Phe Gln Lys
303 385          390          395          400
305 Glu Phe Ala Gly Ala Leu Ser Leu Ala Asp Ala Ala Val Val Leu Glu
306          405          410          415
308 Ile Tyr Gly Ala Arg Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile
309          420          425          430
311 Ile Thr Asp Ala Met Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser
312          435          440          445
314 Ala Val Pro Glu Arg Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val
315          450          455          460
317 Leu Thr Met Gly Ala Gly Ser Val Thr Met Leu Ala Pro Glu Ile Leu
318 465          470          475          480
320 Asp Gln Leu Gln Asn Asn
321          485
324 <210> SEQ ID NO: 3
325 <211> LENGTH: 1539
326 <212> TYPE: DNA
327 <213> ORGANISM: Corynebacterium glutamicum
329 <220> FEATURE:
330 <221> NAME/KEY: CDS
331 <222> LOCATION: (101)..(1516)
332 <223> OTHER INFORMATION: RXA02705
334 <400> SEQUENCE: 3
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337 ttacagcgac tggctccact tagcggaggt ataaataatt atg ggt tct ctg tcc 115
338                                     Met Gly Ser Leu Ser
339                                     1 5
341 cat tta cct cag gcg ctg cag ggc cgt att ctt gtg gcc ggc gct ggt 163
342 His Leu Pro Gln Ala Leu Gln Gly Arg Ile Leu Val Ala Gly Ala Gly
343          10          15          20
345 gtt tcc ggc ctg tcc att gca aag atg ctc agt gag ttg cat tgc gat 211
346 Val Ser Gly Leu Ser Ile Ala Lys Met Leu Ser Glu Leu His Cys Asp

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:29132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:315
L:34115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:387
L:37091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:425
L:37134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:427
L:37136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:427